

FIGURE 1

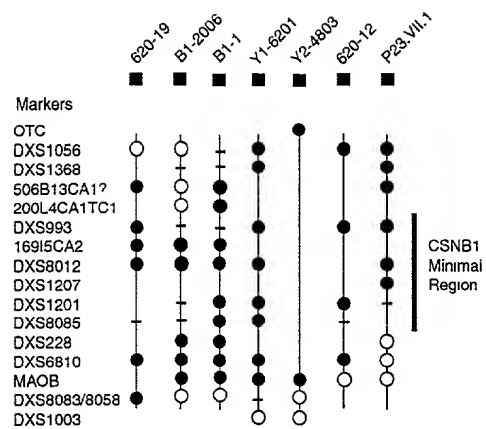
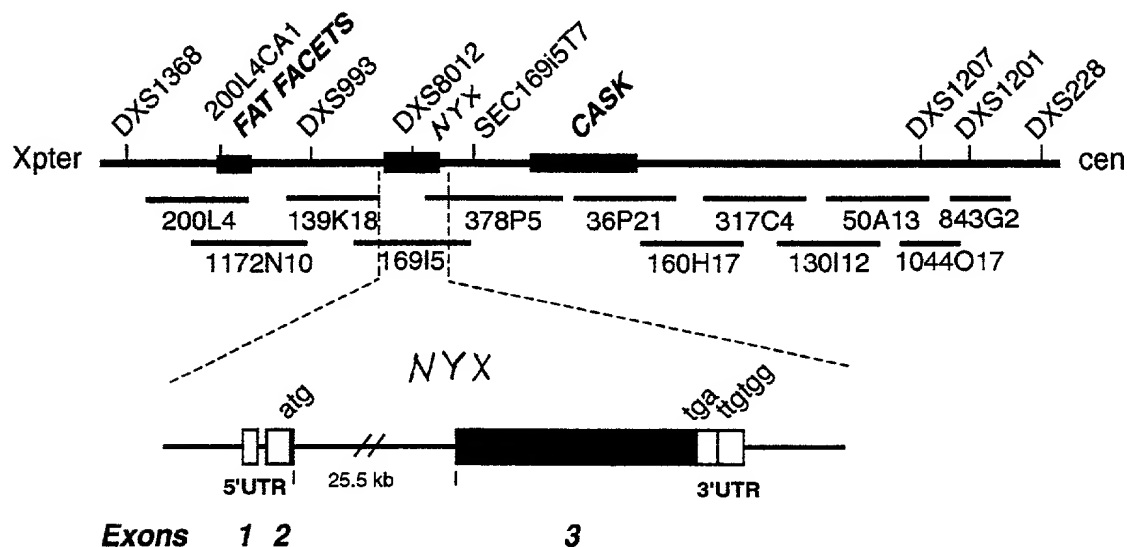


FIGURE 2

a Physical map of the CSNB1 minimal region and genomic organization of *NYX*



b Leucine-rich repeats and the distribution of mutations in the Nyctalopin protein

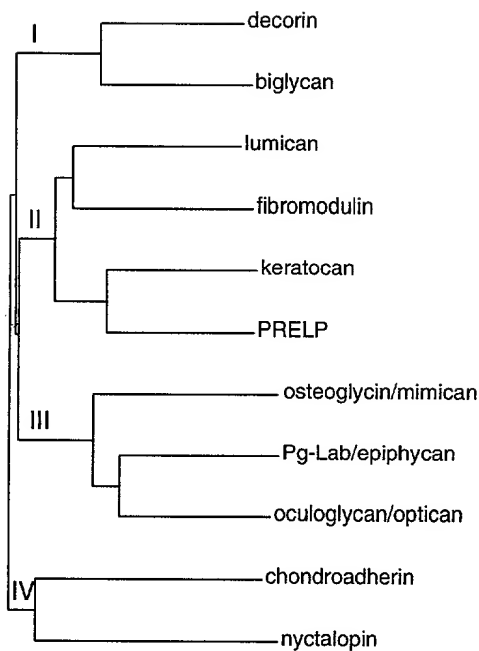
	MKGRGMLVLLLLHAVVLGLPSAWAVGA	ARA PAA A	STVERG	SVR	DR	- 50
		del				
1.	AGLLRVPAELPCEAVSIDLDRNGL					- 74
2.	RFLGERAFGTLPSLRRLSLRHNNL					- 98
3.	SFITPGAFKGLPRLAELRLAHNGDL					- 123
4.	RYLHARTFAALSRLRRDLAACRL					- 147
5.	FSVPERLLAELPALRELAAFDNLFRRVPGALRGL					- 181
6.	ANLTHAHL15LRRLRSLSLQANRV					- 218
	ERGRIEAVASSSLOQ					
7.	RAVHAGAFGDCGVLEHLLLNNDNLL					- 242
8.	AELPADAFRGLRRLRTLNLGGNAL					- 266
9.	DRVARAWFADLAELLEYLDRNSI					- 290
10.	AFVEEGAQNLSGLLALHLNGNRL					- 314
11.	TVLAWVAFQPGFFLGRLLFLFRNPW					- 338
	β-sheet	α-helix				
	LDRLLEWLRLDWMEGSGRVTDVP	ASPGSVAGLDLSQVTFGRSSDGL	VD			- 388
	PEELNLTTSSPGPSPEPAATTVS	RFSLLSKLLAPRVVVEEAANTTGGLA				- 438
	NASLSDSLSSRGVGGAGRQPWFLLASCLLP	SVAQHVVFGQLQMD				- 481

^ insertions of SVPERLL, GLR and RLR, respectively
 v most likely signal peptide cleavage site

FIGURE 3

FIGURE 3
CONT.

c



d

30	40	50	60	70	80
NYX	ACPAACACSTVERGCSVRCDRAGLRVPAELPCEAVSIDLDRNGRELGERAFGTLPSLR				
CHAD	ACPQNCCHSDLOHVICDKVGLQKIP-KVSEKTKLLNLQRNNPEVLAANSFRAMPNLV				
	30	40	50	60	70
90	100	110	120	130	140
NYX	ELSLRHNNLSFTTPGAFKGLRLAELELAHNGDLRYLHARTFAALSRLRLDLAACRLFS				
CHAD	SLHLQHCOIREVAAGAFRLKQITLYLYLSEN-DIRVVYRAGAFDDLTELTYLYLDHNKV--				
	80	90	100	110	120
150	160	170	180	190	200
NYX	VPERLLAELPALRELAAFDNLPRVPCALRGLANLTHAHLERGRTEAVASSSQGLRLRLR				
CHAD	-----TELPR-----GILLSPLVNLRILOINNNKIRELRAGFPQGAQDLR				
	140	150	160	170	
210	220	230	240	250	260
NYX	SLSLQANRVRAVHAGAFGDCGVLEHLLNDNLLAEIPADAFGLRLRLTLNLGGNALDRV				
CHAD	WLYLSENALSSLOPGALDDVENLAKPHVDNRQSSYPASAALSKLRVVEELKLSHNPLKSI				
	180	190	200	210	220
270	280	290	300	310	320
NYX	ARAWFADLAE-LELLYLDNRNSTAFVEEGAFONLSGLLALHLNGNRITVLAWVAFQPGFFL				
CHAD	PDNAFQSFGRYLEPLWLDNTNLEKFSDGAFLVPTLKHVHLENMRLNQLP-SNF-PFDSL				
	240	250	260	270	280
330	340	350	360	370	380
NYX	GRILFLFRNPWCCDLRLWLRDWMEGSGRVTDWPCASPGSVAGLDLSQVTFGRS				
CHAD	ETLALTNNPWKCTQLRGLRRWLEAKASRPDATCASPAKFKQGHIRDYDAFRS				
	300	310	320	330	340

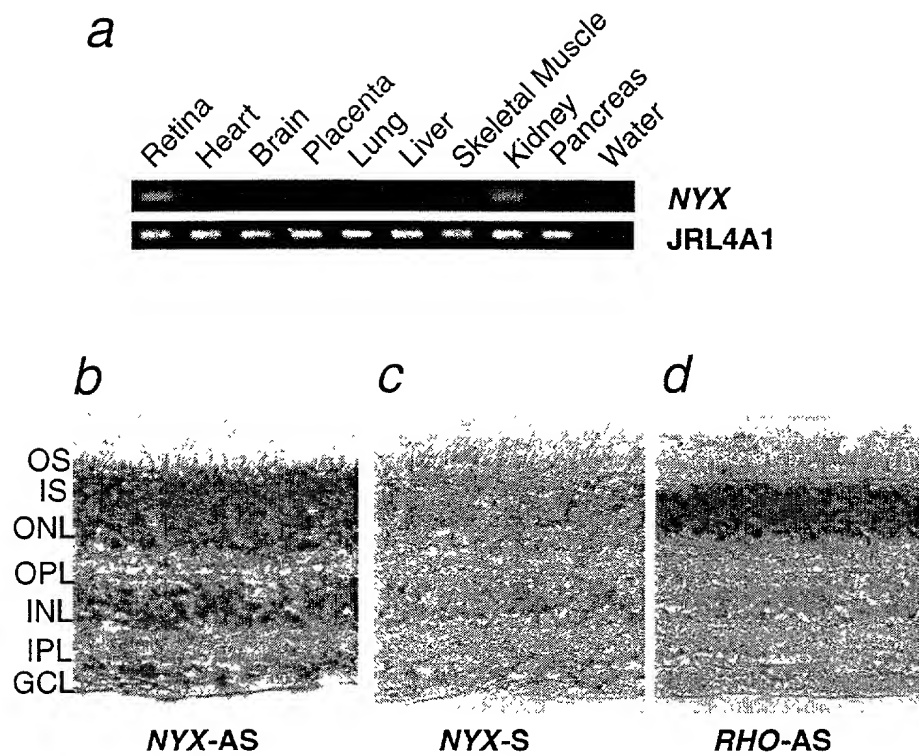
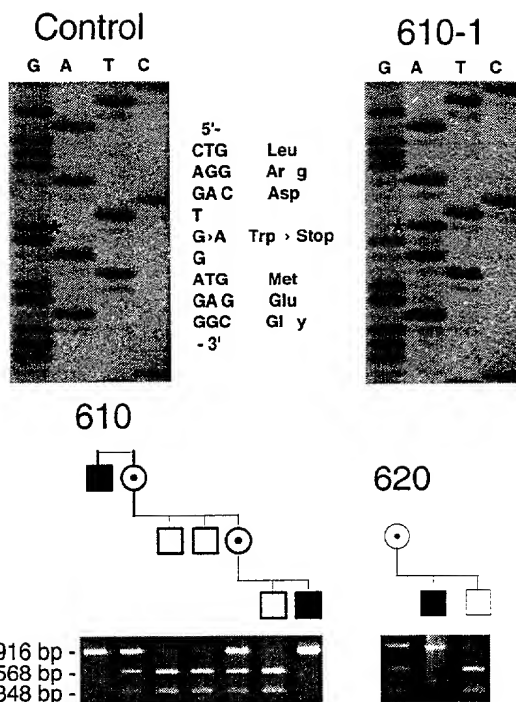
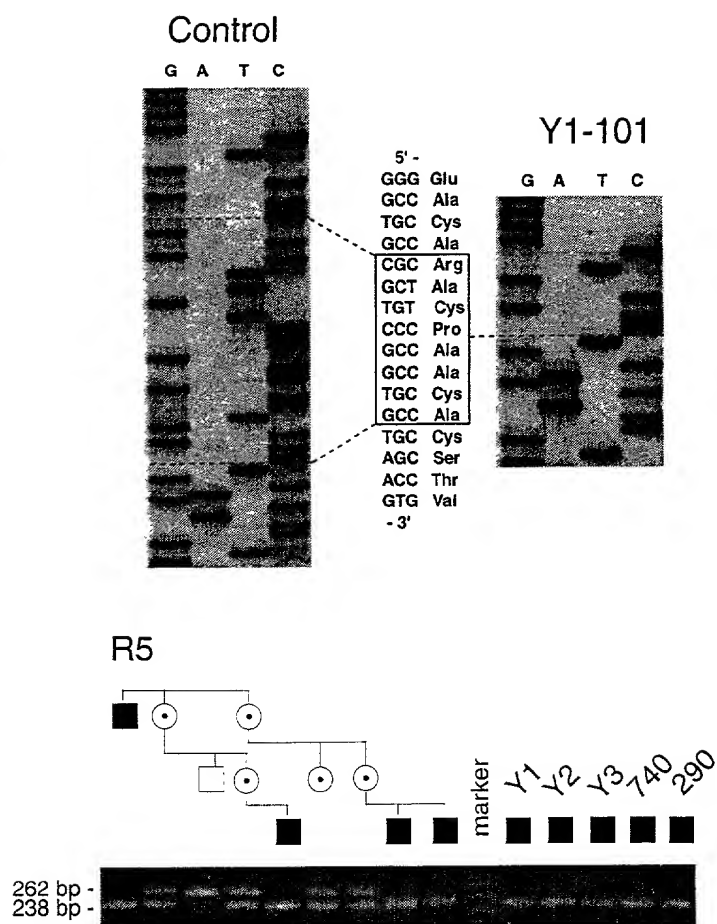


FIGURE 4

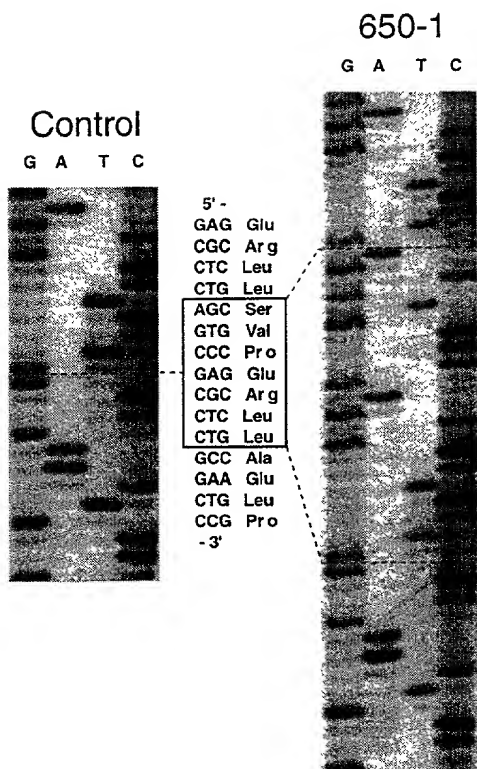
a



b



c



d

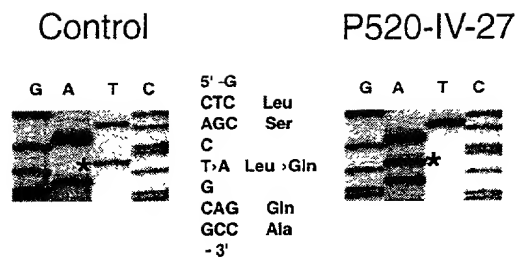


FIGURE 5

Table 1 • Nyctalopin mutations in families with complete CSNB

Family ^a	Origin	Mutation ^b	Codon change	Predicted effect on nyctalopin
290,740,830,Y1,Y2,Y3,R5 ^c USA	USA	85-108del24nt ^d	RACPAACA29-36del	partial loss of N-terminal cysteine cluster
P23.340 (2) (ref 13)	Netherlands	452C>T	P151L	missense, proline to leucine
650 (2)	Canada	464*465ins21nt	SVPERLL155-156ins	expansion of LRR5 ^e
750 ^f (1),780 (1)	Canada,USA	551T>C	L184P	missense, leucine to proline
540 (6)(ref 28, family 2)	Germany	556-618del50ins3nt		frameshift with stop at codon 259
640 (2)	USA	619*620ins9nt	LLR207-208ins	expansion of LRR6
R7 (7)	USA	628*629ins9nt	CLR209-210ins	expansion of LRR6
P520 (2)	Netherlands	638T>A	L213Q	missense, leucine to glutamine
580 (2)	Canada	647A>G	N216S	missense, asparagine to serine
550 (9)(ref 28, family 3)	Germany	695T>C	L232P	missense, leucine to proline
B1 (3)	USA	792C>G	N264K	missense, asparagine to lysine
B660 (1)	USA	854T>C	L285P	missense, leucine to proline
B2 (5)	USA	893T>C	F298S	missense, phenylalanine to serine
610, 620 (4,10)	Costa Rica	1049G>A	W350X	protein truncation, loss of GPI-anchoring

^a families Y1, Y2, Y3, R5, R7, B1 and B2 were first reported in reference 25. Earlier reports on other families is indicated following the family designation.

^b following the recommendations of Nomenclature Working Group.

^c number of affected males in these families: 8, 1, 4, 8, 2 and 5, respectively. For all other families in this table this information is shown in first set of parentheses following the family designation.

^d in the analysis of X chromosomes with this deletion, we observed identical haplotypes across Xp11.4 from DXS556 to DXS228 with some chromosomes diverging proximally or distally beyond this region (15 markers tested)

^e LRR, leucine-rich repeat.

^f Patient 1, whose electrophysiological results are shown in Fig. 1.

FIGURE 6

FIGURE 7